



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/755,466

DATE: 09/17/2004

TIME: 10:41:44

Input Set : N:\Crf3\RULE60\10755466.raw

Output Set: N:\CRF4\09172004\J755466.raw

1 <110> APPLICANT: HIDAKA , Jun et al.
 2 <120> TITLE OF INVENTION: RECOMBINANT HUMAN SM-11044-BINDING RECEPTOR PROTEINS
 EXHIBITING LIGAND-

3 BINDING ACTIVITIES, AND THEIR USES

4 <130> FILE REFERENCE: 0020-4827P

5 <140> CURRENT APPLICATION NUMBER: US/10/755,466

6 <141> CURRENT FILING DATE: 2004-01-13

7 <150> PRIOR APPLICATION NUMBER: US/09/786,681

8 <151> PRIOR FILING DATE: 2001-04-30

9 <160> NUMBER OF SEQ ID NOS: 7

10 <170> SOFTWARE: PatentIn version 3.0

12 <210> SEQ ID NO: 1

13 <211> LENGTH: 2072

14 <212> TYPE: DNA

15 <213> ORGANISM: Homo sapiens

16 <220> FEATURE:

17 <221> NAME/KEY: CDS

18 <222> LOCATION: (49)..(1794)

19 <400> SEQUENCE: 1

20 ggatccacta gtaacggccg ccagtggtgct ggaattctgc agatctag atg cat gct 57
 21 Met His Ala
 22 1
 23 cga gcg gcc gcc gcg ctg tgg ctg ctg ctg ctg ctg ccc cgg acc 105
 24 Arg Ala Ala Ala Ala Leu Trp Leu Leu Leu Leu Leu Leu Pro Arg Thr
 25 5 10 15
 26 cgg gcg gac gag cac gaa cac acg tat caa gat aaa gag gaa gtt gtc 153
 27 Arg Ala Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val
 28 20 25 30 35
 29 tta tgg atg aat act gtt ggg ccc tac cat aat cgt caa gaa aca tat 201
 30 Leu Trp Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr
 31 40 45 50
 32 aag tac ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa agt atc agt 249
 33 Lys Tyr Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser
 34 55 60 65
 35 cat tac cat gaa act ctg gga gaa gca ctt caa ggg gtt gaa ttg gaa 297
 36 His Tyr His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu
 37 70 75 80
 38 ttt agt ggt ctg gat att aaa ttt aaa gat gat gtg atg cca gcc act 345
 39 Phe Ser Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr
 40 85 90 95
 41 tac tgt gaa att gat tta gat aaa gaa aag aga gat gca ttt gta tat 393
 42 Tyr Cys Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr
 43 100 105 110 115
 44 gcc ata aaa aat cat tac tgg tac cag atg tac ata gat gat tta cca 441

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45	Ala Ile Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro	
46	120 125 130	
47	ata tgg ggt att gtt ggt gag gct gat gaa aat gga gaa gat tac tat	489
48	Ile Trp Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr	
49	135 140 145	
50	ctt tgg acc tat aaa aaa ctt gaa ata ggt ttt aat gga aat cga att	537
51	Leu Trp Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile	
52	150 155 160	
53	gtt gat gtt aat cta act agt gaa gga aag gtg aaa ctg gtt cca aat	585
54	Val Asp Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn	
55	165 170 175	
56	act aaa atc cag atg tca tat tca gta aaa tgg aaa aag tca gat gtg	633
57	Thr Lys Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val	
58	180 185 190 195	
59	aaa ttt gaa gat cga ttt gac aaa tat ctt gat ccg tcc ttt ttt caa	681
60	Lys Phe Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln	
61	200 205 210	
62	cat cgg att cat tgg ttt tca att ttc aac tcc ttc atg atg gtg atc	729
63	His Arg Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile	
64	215 220 225	
65	ttc ttg gtg ggc tta gtt tca atg att tta atg aga aca tta aga aaa	777
66	Phe Leu Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys	
67	230 235 240	
68	gat tat gct cgg tac agt aaa gag gaa gaa atg gat gat atg gat aga	825
69	Asp Tyr Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg	
70	245 250 255	
71	gac cta gga gat gaa tat gga tgg aaa cag gtg cat gga gat gta ttt	873
72	Asp Leu Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe	
73	260 265 270 275	
74	aga cca tca agt cac cca ctg ata ttt tcc tct ctg att ggt tct gga	921
75	Arg Pro Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly	
76	280 285 290	
77	tgt cag ata ttt gct gtg tct ctc atc gtt att att gtt gca atg ata	969
78	Cys Gln Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile	
79	295 300 305	
80	gaa gat tta tat act gag agg gga tca atg ctc agt aca gcc ata ttt	1017
81	Glu Asp Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe	
82	310 315 320	
83	gtc tat gct gct acg tct cca gtg aat ggt tat ttt gga gga agt ctg	1065
84	Val Tyr Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu	
85	325 330 335	
86	tat gct aga caa gga gga agg aga tgg ata aag cag atg ttt att ggg	1113
87	Tyr Ala Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly	
88	340 345 350 355	
89	gca ttc ctt atc cca gct atg gtg tgt ggc act gcc ttc ttc atc aat	1161
90	Ala Phe Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn	
91	360 365 370	
92	ttc ata gcc att tat tac cat gct tca aga gcc att cct ttt gga aca	1209
93	Phe Ile Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr	

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94          375          380          385
95  atg gtg gcc gtt tgt tgc atc tgt ttt ttt gtt att ctt cct cta aat 1257
96  Met Val Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn
97          390          395          400
98  ctt gtt ggt aca ata ctt ggc cga aat ctg tca ggt cag ccc aac ttt 1305
99  Leu Val Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe
100         405         410         415
101  cct tgt cgt gtc aat gct gtg cct cgt cct ata ccg gag aaa aaa tgg 1353
102  Pro Cys Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp
103         420         425         430         435
104  ttc atg gag cct gcg gtt att gtt tgc ctg ggt gga att tta cct ttt 1401
105  Phe Met Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe
106          440          445          450
107  ggt tca atc ttt att gaa atg tat ttc atc ttc acg tct ttc tgg gca 1449
108  Gly Ser Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala
109          455          460          465
110  tat aag atc tat tat gtc tat ggc ttc atg atg ctg gtg ctg gtt atc 1497
111  Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile
112          470          475          480
113  ctg tgc att gtg act gtc tgt gtg act att gtg tgc aca tat ttt cta 1545
114  Leu Cys Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu
115          485          490          495
116  cta aat gca gaa gat tac cgg tgg caa tgg aca agt ttt ctc tct gct 1593
117  Leu Asn Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala
118          500          505          510          515
119  gca tca act gca atc tat gtt tac atg tat tcc ttt tac tac tat ttt 1641
120  Ala Ser Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe
121          520          525          530
122  ttc aaa aca aag atg tat ggc tta ttt caa aca tca ttt tac ttt gga 1689
123  Phe Lys Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly
124          535          540          545
125  tat atg gcg gta ttt agc aca gcc ttg ggg ata atg tgt gga gcg att 1737
126  Tyr Met Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile
127          550          555          560
128  ggt tac atg gga aca agt gcc ttt gtc cga aaa atc tat act aat gtg 1785
129  Gly Tyr Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val
130          565          570          575
131  aaa att gac tagagacca agaaaacctg gaactttgga tcaatttctt 1834
132  Lys Ile Asp
133          580
134  tttcataggg gtggaacttg cacagcaaaa acaaacaaac gcaagaagag atttgggctt 1894
135  taactttttt tttttttttt tttttttttt tttttttttt tacgaatgag gcaatttatt 1954
136  aaccagcat ggttgttct aatgcttctt gttggcagct gccacctgtc cggcgattct 2014
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139 <210> SEQ ID NO: 2
140 <211> LENGTH: 582
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
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144 Met His Ala Arg Ala Ala Ala Leu Trp Leu Leu Leu Leu Leu Leu
145 1 5 10 15
146 Pro Arg Thr Arg Ala Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu
147 20 25 30
148 Glu Val Val Leu Trp Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln
149 35 40 45
150 Glu Thr Tyr Lys Tyr Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys
151 50 55 60
152 Ser Ile Ser His Tyr His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val
153 65 70 75 80
154 Glu Leu Glu Phe Ser Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met
155 85 90 95
156 Pro Ala Thr Tyr Cys Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala
157 100 105 110
158 Phe Val Tyr Ala Ile Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp
159 115 120 125
160 Asp Leu Pro Ile Trp Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu
161 130 135 140
162 Asp Tyr Tyr Leu Trp Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly
163 145 150 155 160
164 Asn Arg Ile Val Asp Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu
165 165 170 175
166 Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys
167 180 185 190
168 Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser
169 195 200 205
170 Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met
171 210 215 220
172 Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile Leu Met Arg Thr
173 225 230 235 240
174 Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp
175 245 250 255
176 Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly
177 260 265 270
178 Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile
179 275 280 285
180 Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile Val Ile Val
181 290 295 300
182 Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr
183 305 310 315 320
184 Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly
185 325 330 335
186 Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met
187 340 345 350
188 Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe
189 355 360 365
190 Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro
191 370 375 380
192 Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu

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Input Set : N:\Crif3\RULE60\10755466.raw

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193	385	390	395	400
194	Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln			
195		405	410	415
196	Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu			
197		420	425	430
198	Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile			
199		435	440	445
200	Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser			
201		450	455	460
202	Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val			
203		465	470	475
204	Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr Ile Val Cys Thr			
205		485	490	495
206	Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe			
207		500	505	510
208	Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr			
209		515	520	525
210	Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe			
211		530	535	540
212	Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys			
213		545	550	555
214	Gly Ala Ile Gly Tyr Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr			
215		565	570	575
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222	<213> ORGANISM: Homo sapiens			
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225	<222> LOCATION: (11)..(1747)			
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230	ccc cgg acc cgg gcg gac gag cac gaa cac acg tat caa gat aaa gag			97
231	Pro Arg Thr Arg Ala Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu			
232	15 20 25			
233	gaa gtt gtc tta tgg atg aat act gtt ggg ccc tac cat aat cgt caa			145
234	Glu Val Val Leu Trp Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln			
235	30 35 40 45			
236	gaa aca tat aag tac ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa			193
237	Glu Thr Tyr Lys Tyr Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys			
238	50 55 60			
239	agt atc agt cat tac cat gaa act ctg gga gaa gca ctt caa ggg gtt			241
240	Ser Ile Ser His Tyr His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val			
241	65 70 75			
242	gaa ttg gaa ttt agt ggt ctg gat att aaa ttt aaa gat gat gtg atg			289

RAW SEQUENCE LISTING ERROR SUMMARY

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Output Set: N:\CRF4\09172004\J755466.raw

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The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2

Seq#:7; Line(s) 442

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/755,466

DATE: 09/17/2004

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